

## SEQUENCE LISTING

<110> The Government of the United States of America as represented by the Secretary of the Department of Health and Human Services  
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Pastan, Ira H.  
Lee, Byungkook

<120> GENE EXPRESSED IN PROSTATE CANCER AND METHODS OF USE

<130> 4239-68223

<150> 60/461,399  
<151> 2003-04-08

<160> 12

<170> PatentIn version 3.2

<210> 1  
<211> 933  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Splice Variant-Novel Gene Expressed in Prostate

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Pro Thr Leu Cys Pro Ala Val Arg Thr Gly Leu Tyr Cys Arg Asp Gln  
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Ala His Ala Glu Arg Trp Ala Met Thr Ser Glu Thr Ser Ser Gly Ser  
35 40 45

His Cys Ala Arg Ser Arg Met Leu Arg Arg Arg Ala Gln Glu Glu Asp  
50 55 60

Ser Thr Val Leu Ile Asp Val Ser Pro Pro Glu Ala Glu Lys Arg Gly  
65 70 75 80

Ser Tyr Gly Ser Thr Ala His Ala Ser Glu Pro Gly Gly Gln Gln Ala  
85 90 95

Ala Ala Cys Arg Ala Gly Ser Pro Ala Lys Pro Arg Ile Ala Asp Phe  
100 105 110

Val Leu Val Trp Glu Glu Asp Leu Lys Leu Asp Arg Gln Gln Asp Ser  
115 120 125

Ala Ala Arg Asp Arg Thr Asp Met His Arg Thr Trp Arg Glu Thr Phe  
130 135 140

Leu Asp Asn Leu Arg Ala Ala Gly Leu Cys Val Asp Gln Gln Asp Val  
145 150 155 160

Gln Asp Gly Asn Thr Thr Val His Tyr Ala Leu Leu Ser Ala Ser Trp  
165 170 175

Ala Val Leu Cys Tyr Tyr Ala Glu Asp Leu Arg Leu Lys Leu Pro Leu  
180 185 190

Gln Glu Leu Pro Asn Gln Ala Ser Asn Trp Ser Ala Gly Leu Leu Ala  
195 200 205

Trp Leu Gly Ile Pro Asn Val Leu Leu Glu Val Val Pro Asp Val Pro  
210 215 220

Pro Glu Tyr Tyr Ser Cys Arg Phe Arg Val Asn Lys Leu Pro Arg Phe  
225 230 235 240

Leu Gly Ser Asp Asn Gln Asp Thr Phe Phe Thr Ser Thr Lys Arg His  
245 250 255

Gln Ile Leu Phe Glu Ile Leu Ala Lys Thr Pro Tyr Gly His Glu Lys  
260 265 270

Lys Asn Leu Leu Gly Ile His Gln Leu Leu Ala Glu Gly Val Leu Ser  
275 280 285

Ala Ala Phe Pro Leu His Asp Gly Pro Phe Lys Thr Pro Pro Glu Gly  
290 295 300

Pro Gln Ala Pro Arg Leu Asn Gln Arg Gln Val Leu Phe Gln His Trp  
305 310 315 320

Ala Arg Trp Gly Lys Trp Asn Lys Tyr Gln Pro Leu Asp His Val Arg  
325 330 335

Arg Tyr Phe Gly Glu Lys Val Ala Leu Tyr Phe Ala Trp Leu Gly Phe  
340 345 350

Tyr Thr Gly Trp Leu Leu Pro Ala Ala Val Val Gly Thr Leu Val Phe  
355 360 365

Leu Val Gly Cys Phe Leu Val Phe Ser Asp Ile Pro Thr Gln Glu Leu  
 370 375 380

Cys Gly Ser Lys Asp Ser Phe Glu Met Cys Pro Leu Cys Leu Asp Cys  
 385 390 395 400

Pro Phe Trp Leu Leu Ser Ser Ala Cys Ala Leu Ala Gln Ala Gly Arg  
 405 410 415

Leu Phe Asp His Gly Gly Thr Val Phe Phe Ser Leu Phe Met Ala Leu  
 420 425 430

Trp Ala Val Leu Leu Glu Tyr Trp Lys Arg Lys Ser Ala Thr Leu  
 435 440 445

Ala Tyr Arg Trp Asp Cys Ser Asp Tyr Glu Asp Thr Glu Glu Arg Pro  
 450 455 460

Arg Pro Gln Phe Ala Ala Ser Ala Pro Met Thr Ala Pro Asn Pro Ile  
 465 470 475 480

Thr Gly Glu Asp Glu Pro Tyr Phe Pro Glu Arg Ser Arg Ala Arg Arg  
 485 490 495

Met Leu Ala Gly Ser Val Val Ile Val Val Met Val Ala Val Val Val  
 500 505 510

Met Cys Leu Val Ser Ile Ile Leu Tyr Arg Ala Ile Met Ala Ile Val  
 515 520 525

Val Ser Arg Ser Gly Asn Thr Leu Leu Ala Ala Trp Ala Ser Arg Ile  
 530 535 540

Ala Ser Leu Thr Gly Ser Val Val Asn Leu Val Phe Ile Leu Ile Leu  
 545 550 555 560

Ser Lys Ile Tyr Val Ser Leu Ala His Val Leu Thr Arg Trp Glu Met  
 565 570 575

His Arg Thr Gln Thr Lys Phe Glu Asp Ala Phe Thr Leu Lys Val Phe  
 580 585 590

Ile Phe Gln Phe Val Asn Phe Tyr Ser Ser Pro Val Tyr Ile Ala Phe  
 595 600 605

Phe Lys Gly Arg Phe Val Gly Tyr Pro Gly Asn Tyr His Thr Leu Phe

610

615

620

Gly Val Arg Asn Glu Glu Cys Ala Ala Gly Gly Cys Leu Ile Glu Leu  
625 630 635 640

Ala Gln Glu Leu Leu Val Ile Met Val Gly Lys Gln Val Ile Asn Asn  
645 650 655

Met Gln Glu Val Leu Ile Pro Lys Leu Lys Gly Trp Trp Gln Lys Phe  
660 665 670

Arg Leu Arg Ser Lys Lys Arg Lys Ala Gly Ala Ser Ala Gly Ala Ser  
675 680 685

Gln Gly Pro Trp Glu Asp Asp Tyr Glu Leu Val Pro Cys Glu Gly Leu  
690 695 700

Phe Asp Glu Tyr Leu Glu Met Val Leu Gln Phe Gly Phe Val Thr Ile  
705 710 715 720

Phe Val Ala Ala Cys Pro Leu Ala Pro Leu Phe Ala Leu Leu Asn Asn  
725 730 735

Trp Val Glu Ile Arg Leu Asp Ala Arg Lys Phe Val Cys Glu Tyr Arg  
740 745 750

Arg Pro Val Ala Glu Arg Ala Gln Asp Ile Gly Ile Trp Phe His Ile  
755 760 765

Leu Ala Gly Leu Thr His Leu Ala Val Ile Ser Asn Ala Phe Leu Leu  
770 775 780

Ala Phe Ser Ser Asp Phe Leu Pro Arg Ala Tyr Tyr Arg Trp Thr Arg  
785 790 795 800

Ala His Asp Leu Arg Gly Phe Leu Asn Phe Thr Leu Ala Arg Ala Pro  
805 810 815

Ser Ser Phe Ala Ala His Asn Arg Thr Cys Arg Tyr Arg Ala Phe  
820 825 830

Arg Asp Asp Asp Gly His Tyr Ser Gln Thr Tyr Trp Asn Leu Leu Ala  
835 840 845

Ile Arg Leu Ala Phe Val Ile Val Phe Glu His Val Val Phe Ser Val  
850 855 860

Gly Arg Leu Leu Asp Leu Leu Val Pro Asp Ile Pro Glu Ser Val Glu  
 865 870 875 880

Ile Lys Val Lys Arg Glu Tyr Tyr Leu Ala Lys Gln Ala Leu Ala Glu  
 885 890 895

Asn Glu Val Leu Phe Gly Thr Asn Gly Thr Lys Asp Glu Gln Pro Lys  
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Gly Ser Glu Leu Ser Ser His Trp Thr Pro Phe Thr Val Pro Lys Ala  
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Ser Gln Leu Gln Gln  
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<210> 2

<211> 3308

<212> DNA

<213> Artificial Sequence

<220>

<223> Splice Variant-Novel Gene Expressed in Prostate

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| ctccccctgcc  | tgcttcctgg  | cccacttgca  | ggcaagggtga | ggccatgcga | atggctgcca  | 120 |
| ctgcctggc    | ggggctccaa  | gggccaccccc | tccccacccct | ctgtcccgca | gtgaggacgg  | 180 |
| gactctactg   | ccgagaccag  | gctcacgctg  | agaggtggc   | catgacctcc | gagacctctt  | 240 |
| ccggaagcca   | ctgtgccagg  | agcaggatgc  | tgcggcgacg  | ggcccaggaa | gaggacagca  | 300 |
| ccgtcctgtat  | cgatgtgagc  | ccccctgagg  | cagagaagag  | gggctttac  | gggagcacag  | 360 |
| cccacgcctc   | ggagccaggt  | ggacagcaag  | cggccgcctg  | cagagctggg | agtccctgcca | 420 |
| agccccggat   | cgcagacttc  | gtcctcgttt  | gggaggagga  | cctgaagcta | gacaggcagc  | 480 |
| aggacagtgc   | cgcggggac   | agaacagaca  | tgcacaggac  | ctggcgggag | actttctgg   | 540 |
| ataatcttcg   | tgccgcgtgg  | ctgtgtgtag  | accagcagga  | cgtccaggac | gggaacaccca | 600 |
| cagtgcacta   | cgcctcctc   | agcgcctcct  | gggctgtgct  | ctgctactac | gccgaagacc  | 660 |
| tgcgcctgaa   | gctgcccttg  | caggagttac  | ccaaccaggc  | ctccaactgg | tcggccggcc  | 720 |
| tgctggcatg   | gctgggcatc  | cccaacgtcc  | tgctggaggt  | tgtgccagac | gtaccccccgg | 780 |
| agtactactc   | ctgcccgttc  | agagtgaaca  | agctgccacg  | cttcctcggg | agtgacaacc  | 840 |
| aggacacacctt | cttcacaaggc | accaagagggc | accaaattct  | gtttgagatc | ctggccaaga  | 900 |

|  |      |
|--|------|
| ccccgtatgg ccacgagaag aaaaacctgc ttgggatcca ccagctgctg gcagagggtg    | 960  |
| tcctcagtgc cgccctcccc ctgcatgacg gccccttcaa gacgccccca gagggccgc     | 1020 |
| aggctccacg cctcaaccag cgccaagtcc tttccagca ctgggcgcgc tggggcaagt     | 1080 |
| ggaacaagta ccagccccctg gaccacgtgc gcaggtactt cggggagaag gtggccctct   | 1140 |
| acttcgcctg gctcgggttt tacacaggct ggctcctgcc agcggcagtg gtgggcacac    | 1200 |
| tggtgttcct ggtgggctgc ttcctggtgt tctcagacat acccacgcag gaactgtgtg    | 1260 |
| gcagcaagga cagttcgag atgtgcccac tttgcctcga ctgccccttc tggctgctct     | 1320 |
| ccagcgcctg tgccctggcc cagggccggcc ggctgttcga ccacggcggc accgtgttct   | 1380 |
| tcagcttgtt catggcactg tggggcgtgc tgctgctgga gtactggaag cggaagagcg    | 1440 |
| ccacgctggc ctaccgctgg gactgctctg actacgagga cactgaggag aggcctcggc    | 1500 |
| cccagttgc cgcctcagcc cccatgacag ccccgaaccc catcacgggt gaggacgagc     | 1560 |
| cctacttccc tgagaggagc cgcgcgcgc gcatgctggc cggctctgtg gtgatcgtgg     | 1620 |
| tgatggtggc cgtgggggtc atgtgcctcg tgtctatcat cctgtaccgt gccatcatgg    | 1680 |
| ccatcgtggt gtccaggtcg ggcaacaccc ttctcgcagc ctgggcctct cgcatcgcca    | 1740 |
| gcctcacggg gtctgttagtg aacctcgct tcattcctcat cctctccaag atctatgtat   | 1800 |
| ccctggccca cgtcctgaca cgatggaaa tgcaccgcac ccagaccaag ttcgaggacg     | 1860 |
| ccttcacccct caaggtgttc atcttcagg tctgtcaactt ctactcctca cccgtctaca   | 1920 |
| ttgcctctt caagggcagg tttgtggat acccaggcaa ctaccacacc ttgtttggag      | 1980 |
| tccgcaatga ggagtgcgcg gctggaggct gcctgatcga gctggcacag gagctcctgg    | 2040 |
| tcatcatggt gggcaagcag gtcataaca acatgcagga ggtcctcatac ccgaagctaa    | 2100 |
| agggctggtg gcagaagttc cggcttcgct ccaagaagag gaaggcggga gttctgcag     | 2160 |
| gggctagcca gggccctgg gaggacgact atgagcttgt gccctgtgag ggtctgtttg     | 2220 |
| acgagttaccc gaaaatggtg ctgcagttcg gttcgtcac catttcggt gccgcctgtc     | 2280 |
| cgctcgcgcg cgttccgcctc ctgctcaaca actgggtgga gatccgcttg gacgcgcgc    | 2340 |
| atttcggtcg cgagtaccgg cgcctgtgg cggagcgcgc ccaggacatc ggcattctgg     | 2400 |
| tccacatcct ggcgggcctc acgcacccctgg cggtcatacg caacgccttc ctccctggcct | 2460 |
| tctcgtccga ctccctgccc cgcgcctact accgggtggac cccgcacccac gacctgcgcg  | 2520 |
| gtttcctcaa cttcacgctg ggcgcagccc cgttccctt cggccgcgcg cacaaccgca     | 2580 |
| cgtcaggtta tcgggctttc cgggatgacg atggacatata ttcccagacc tactggaatc   | 2640 |
| ttcttgcacat cgcctggcc ttcgtcattt gttttgagca tgggttttc tccgttggcc     | 2700 |
| gcctcctggaa ctcctgggtg cctgacatcc cagagtctgt ggagatcaaa gtgaagcggg   | 2760 |

|            |             |            |            |             |            |      |
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| agtactacct | ggctaagcag  | gcactggctg | agaatgaggt | tcttttggaa  | acgaacggaa | 2820 |
| caaaggatga | gcagcccaag  | ggctcagagc | ttagtccca  | ctggacacccc | ttcacggttc | 2880 |
| ccaaggccag | ccagctgcag  | cagtgcacgc | tggaaggaca | tctgggtggtc | cttaggggag | 2940 |
| tggccctcc  | tgagccctgc  | gagcagcgtc | ctttccctct | tccctcagggc | agcggctgtg | 3000 |
| tgaaccgctg | gctgctgttg  | tgcctcatct | ctgggcacat | tgcctgcttc  | cccccagcgc | 3060 |
| cggcttctct | cctcagagcg  | cctgtcactc | catccccggc | agggagggac  | cgtcagctca | 3120 |
| caaggccctc | tttgcctcct  | gctcccagac | ataagcccaa | ggggccctg   | cacccaaggg | 3180 |
| accctgtccc | tcgggtggcct | ccccaggccc | ctggacacga | cagttctcct  | caggcaggtg | 3240 |
| ggctttgtgg | tcctcgccgc  | ccctggccac | atcgccctct | cctcttacac  | ctggtgacct | 3300 |
| tcgaatgt   |             |            |            |             |            | 3308 |

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&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Splice Variant-Novel Gene Expressed in Prostate

&lt;400&gt; 3

|     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Phe | Met | Ala | Leu | Trp | Ala | Val |
| 1   |     |     |     | 5   |     |     |     |     |

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&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Splice Variant-Novel Gene Expressed in Prostate

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Leu | Glu | Val | Val | Pro | Asp | Val |
| 1   |     |     |     | 5   |     |     |     |     |

&lt;210&gt; 5

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Splice Variant-Novel Gene Expressed in Prostate

&lt;400&gt; 5

Ala Leu Leu Ser Ala Ser Trp Ala Val

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5

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Leu Leu Ala Ile Arg Leu Ala Phe Val  
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Ile Leu Phe Glu Ile Leu Ala Lys Thr  
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Trp Leu Leu Ser Ser Ala Cys Ala Leu  
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<212> PRT

<213> Artificial Sequence

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<223> Splice Variant-Novel Gene Expressed in Prostate

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Lys Ile Tyr Val Ser Leu Ala His Val  
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<212> DNA

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<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer/probe

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22